

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2001, 08:03:35 ; Search time 5355.78 Seconds
(without alignments)
17816.367 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169
Sequence: 1 atctgtgtcagtttaccctc.....ctgtgtccctccatgtcag 6169

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba1:*
- 2: gb_ba2:*
- 3: gb_ba3:*
- 4: gb_in1:*
- 5: gb_in2:*
- 6: gb_in3:*
- 7: gb_om:*
- 8: gb_ov:*
- 9: gb_pat1:*
- 10: gb_pat2:*
- 11: gb_ph:*
- 12: gb_pl1:*
- 13: gb_pl2:*
- 14: gb_pl3:*
- 15: gb_pl4:*
- 16: em_ba1:*
- 17: em_ba2:*
- 18: em_fun:*
- 19: em_htgo_hum:*
- 20: em_htgo_inv:*
- 21: em_htgo_rod:*
- 22: em_htg_hum1:*
- 23: em_htg_hum2:*
- 24: em_htg_hum3:*
- 25: em_htg_hum4:*
- 26: em_htg_hum5:*
- 27: em_htg_hum6:*
- 28: em_htg_hum7:*
- 29: em_htg_hum8:*
- 30: em_htg_inv1:*
- 31: em_htg_inv2:*
- 32: em_htg_other:*
- 33: em_htg_rod:*
- 34: em_hum1:*
- 35: em_hum2:*
- 36: em_hum3:*
- 37: em_hum4:*
- 38: em_hum5:*
- 39: em_hum6:*
- 40: em_hum7:*
- 41: em_in:*
- 42: em_om:*
- 43: em_or:*

44: em_ov:*

45: em_pat:*

46: em_ph:*

47: em_pl:*

48: em_ro:*

49: em_sts:*

50: em_sy:*

51: em_un:*

52: em_vl:*

53: gb_sts1:*

54: gb_sts2:*

55: gb_sts3:*

56: gb_sy:*

57: gb_un:*

58: gb_vl1:*

59: gb_vl2:*

60: gb_htg1:*

61: gb_htg2:*

62: gb_htg3:*

63: gb_htg4:*

64: gb_htg5:*

65: gb_htg6:*

66: gb_htg7:*

67: gb_htg8:*

68: gb_htg9:*

69: gb_htg10:*

70: gb_htg11:*

71: gb_htg12:*

72: gb_htg13:*

73: gb_htg14:*

74: gb_htg15:*

75: gb_htg16:*

76: gb_htg17:*

77: gb_htg18:*

78: gb_htg19:*

79: gb_htg20:*

80: gb_htg21:*

81: gb_htg22:*

82: gb_htg23:*

83: gb_htg24:*

84: gb_htg25:*

85: gb_pr1:*

86: gb_pr2:*

87: gb_pr3:*

88: gb_pr4:*

89: gb_pr5:*

90: gb_pr6:*

91: gb_pr7:*

92: gb_pr8:*

93: gb_pr9:*

94: gb_fo1:*

95: gb_fo2:*

96: gb_in4:*

97: gb_pr10:*

98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6105.4	99.0	79376	92 HS454G6	2398750 Human DNA s
2	6054.4	98.1	170425	68 AC024490	AC024490 Homo sapi
3	5300	85.9	5300	88 AF007562	AF007562 Homo sapi
4	2677.4	43.4	2800	93 HSMYOC1	AF049791 Homo sapi
5	1190.4	19.3	1228	85 AB006686S1	AB006686 Homo sapi
6	1084.4	17.6	1086	93 HSGCL1A1	297171 Homo sapien
7	651.2	10.6	1934	91 D88214	D88214 Homo sapien
8	640.4	10.4	1871	9 AX004457	AX004457 Sequence

9	640.4	10.4	1871	9	AX004474	AX004474 Sequence
10	640.4	10.4	1999	9	AR030962	AR030962 Sequence
11	640.4	10.4	1999	9	AR066022	AR066022 Sequence
12	640.4	10.4	1999	9	AR069089	AR069089 Sequence
13	640.4	10.4	2000	97	HSU85257	HSU85257 Human trabe
14	640.4	10.4	2002	9	AB4847	AB4847 Sequence 2
15	635.6	10.3	2000	9	AB4850	AB4850 Sequence 2
16	626.4	10.2	2001	93	HSAP001620	HSAP001620 Homo sapi
17	604.4	9.8	1512	9	AB4848	AB4848 Sequence 3
18	604.4	9.8	1512	9	AR030963	AR030963 Sequence
19	604.4	9.8	1512	9	AR066023	AR066023 Sequence
20	604.4	9.8	1512	9	AR069090	AR069090 Sequence
21	599.6	9.7	1512	9	AB4851	AB4851 Sequence 3
22	585.8	9.5	2800	94	MMUSWOC1	MMUSWOC1 Sequence 3
23	559	9.1	1016	94	MMWTIGP1	MMWTIGP1 Sequence 3
24	556.6	9.0	1969	9	AR020502	AR020502 Sequence 2
25	556.6	9.0	1969	10	I36470	I36470 Sequence 2
26	519.6	8.4	1491	9	AR020503	AR020503 Sequence 3
27	519.6	8.4	1491	10	I36471	I36471 Sequence 3
28	440.8	7.1	2004	94	AB013592	AB013592 Mus muscu
29	440.8	7.1	2059	94	AF039869	AF039869 Mus muscu
30	430.4	7.0	2044	94	AB019393	AB019393 Rattus no
31	426.2	6.9	2068	94	AF093567	AF093567 Rattus no
32	398.8	6.5	1473	7	AB027758	AB027758 Bos tauru
33	217	3.5	228	88	AF007564	AF007564 Homo sapi
34	189.8	3.1	161577	86	AC007688	AC007688 Homo sapi
35	189	3.1	214540	62	AC012404	AC012404 Homo sapi
36	187.8	3.0	97037	85	AC004973	AC004973 Homo sapi
37	187.8	3.0	135038	97	HUWYKXD703	HUWYKXD703 Homo sapi
38	187.6	3.0	187376	76	AC029767	AC029767 Homo sapi
39	187.6	3.0	193267	61	AC009409	AC009409 Homo sapi
40	187.4	3.0	139776	90	AL160165	AL160165 Human DNA
41	185.8	3.0	76727	92	HS821D11	HS821D11 Human DNA
42	185.8	3.0	151994	70	AC026395	AC026395 Homo sapi
43	185.8	3.0	156958	69	AC025947	AC025947 Homo sapi
44	185.8	3.0	161499	63	AC015488	AC015488 Homo sapi
45	185.8	3.0	183216	79	AL161726	AL161726 Homo sapi

ALIGNMENTS

RESULT	1	HS454G6	79376 bp	DNA	PRI	23-NOV-1999
LOCUS	HS454G6/c	Human DNA sequence from PAC 454G6 on chromosome 1q24. Contains				
DEFINITION		trabecular meshwork inducible glucocorticoid response protein,				
		TIGR, myocillin, ESTs and STS.				
ACCESSION		298750				
VERSION		298750.1	GI:2887277			
KEYWORDS		1q24; myocillin; TIGR.				
SOURCE		human.				
ORGANISM		Homo sapiens				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
		Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE		1 (bases 1 to 79376)				
AUTHORS		Deadman,R.				
TITLE		Direct Submision				
JOURNAL		Submitted (27-OCT-1997) Chromosome 1 Project Group				
		(http://www.sanger.ac.uk/HGP/Chrl1) Sanger Centre, Hinxton,				
		Cambridgeshire, CB10 1SA, UK. E-mail enquiries:				
		humfrey@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk				
		On Feb 14, 1998 this sequence version replaced gi:2465060.				
COMMENT		IMPORTANT: This sequence is not the entire insert of clone 454G6.				
		It may be shorter because we only sequence overlapping sections				
		once, or longer because we arrange for a small overlap between				
		neighbouring submisions.				
		During sequence assembly data is compared from overlapping clones.				
		Where differences are found these are annotated as variations				
		together with a note of the overlapping clone name. Note that the				
		variations annotated may not be found in the sequence submission				
		corresponding to the overlapping clone as we submit sequences with				
		only a small overlap as described above.				

FEATURES

source	This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl1/
repeat_region	This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
repeat_region	The true left end of clone 454G6 is at 1 in this sequence. The true left end of clone 560B9 is at 79273.
repeat_region	454G6 is from the library RPC13 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.
repeat_region	For further details see http://bacpac.med.buffalo.edu/ .
repeat_region	location/Qualifiers
repeat_region	1..79376
repeat_region	/organism="Homo sapiens"
repeat_region	/db_xref="taxon:9606"
repeat_region	/chromosome="1"
repeat_region	/map="1q24"
repeat_region	/clone="RP3-454G6"
repeat_region	/clone_1lb="RPCT-3"
repeat_region	435..472
repeat_region	/note="19 copies of 2 mer 82 & conserved"
prim_transcript	1914..>3968
prim_transcript	/note="match: multiple ESTs
prim_transcript	match: R56576 AA043968 W61639 F12081 AA046699
prim_transcript	match: R02925 AA131540 W00634 R36066 AA313383
prim_transcript	match: AA163561 F02925 AA131540 W00634 R36066
prim_transcript	match: AA313383 AA163561 N89173 AA174814 AA057059
prim_transcript	match: AA329084 W47082 AA043955 AA341783 AA353681
prim_transcript	match: AA046487 AA369741 H08313 AA186895 H32730
prim_transcript	match: H08333 H08236 N42052 D61944 R27102 N32353
prim_transcript	match: N30491 AA307150 AA192"
repeat_region	3703..3746
repeat_region	/note="22 copies of 2 mer 89 & conserved"
repeat_region	4051..4183
repeat_region	/note="AluSq repeat: matches 1..133 of consensus
repeat_region	incomplete repeat"
repeat_region	4200..4502
repeat_region	/note="AluSq repeat: matches 2..301 of consensus"
repeat_region	4639..4851
repeat_region	/note="AluSx repeat: matches 2..194 of consensus
repeat_region	incomplete repeat"
repeat_region	5216..5345
repeat_region	/note="AluIo repeat: matches 132..1 of consensus
repeat_region	incomplete repeat"
repeat_region	7759..7907
repeat_region	/note="MIR repeat: matches 174..1 of consensus"
repeat_region	7933..9328
repeat_region	/note="TIGER1 repeat: matches 1..1472 of consensus"
repeat_region	9332..9626
repeat_region	/note="AluSg repeat: matches 1..289 of consensus"
repeat_region	9639..10335
repeat_region	/note="TIGER1 repeat: matches 1469..2174 of consensus"
repeat_region	10343..10642
repeat_region	/note="AluSp repeat: matches 1..300 of consensus"
repeat_region	10643..10856
repeat_region	/note="TIGER1 repeat: matches 2175..2417 of consensus"
repeat_region	<10903..>16855
repeat_region	/note="endogenous retroviral sequence"
repeat_region	10949..11384
repeat_region	/note="LTR2 repeat: matches 31..449 of consensus"
repeat_region	15835..15870
repeat_region	/note="18 copies of 2 mer 83 & conserved"
repeat_region	16856..17286
repeat_region	/note="LTR2 repeat: matches 31..449 of consensus"
repeat_region	17287..17574
repeat_region	/note="AluSg repeat: matches 15..300 of consensus"
repeat_region	18294..18650
repeat_region	/note="THE1B repeat: matches 358..1 of consensus"
repeat_region	18877..19180

repeat_region	/note="A1uY repeat: matches 301. .2 of consensus" 19767. .20013 /note="MT12_internal repeat: matches 5002. .4750 of consensus" 20051. .20118
repeat_region	/note="MT1F repeat: matches 539. .471 of consensus 20130. .20261 /note="A1uB repeat: matches 131. .1 of consensus incomplete repeat" 20264. .20722
repeat_region	/note="MT1F repeat: matches 482. .1 of consensus" 20858. .21223 /note="MSTD repeat: matches 394. .1 of consensus" 21216. .21302 /note="MT12_internal repeat: matches 4520. .4433 of consensus" 21403. .21763
repeat_region	/note="MT12_internal repeat: matches 3887. .3580 of consensus" 21978. .22357 /note="MT12_internal repeat: matches 3218. .2839 of consensus" 22363. .22524 /note="MT12_internal repeat: matches 2495. .2317 of consensus" 22531. .22839
repeat_region	/note="A1uX repeat: matches 302. .1 of consensus" 23007. .23309 /note="A1uSp repeat: matches 3. .301 of consensus" 23286. .>23360 /note="STS G07544" complement(23652. .24072) /note="STS G07436" 24008. .24290
repeat_region	/note="A1uO repeat: matches 298. .6 of consensus" 25895. .26364 /note="L1R2 repeat: matches 2. .449 of consensus" 26397. .26697 /note="A1uG repeat: matches 1. .302 of consensus" 26719. .27021
repeat_region	/note="A1uX repeat: matches 1. .302 of consensus" 29037. .29334 /note="A1uX repeat: matches 300. .3 of consensus" 30028. .30310 /note="A1uX repeat: matches 1. .301 of consensus" 30402. .30559
repeat_region	/note="MT12B repeat: matches 264. .404 of consensus 30402. .30615 /note="MT12A repeat: matches 264. .453 of consensus" <30801. .>31136 /note="match: 5' EST AA256902 clone 682136" 30980. .31222
repeat_region	/note="M1R4B repeat: matches 199. .431 of consensus 31232. .31588 /note="A1uC repeat: matches 299. .1 of consensus" 31530. .31654 /note="M1R4B repeat: matches 417. .540 of consensus 31836. .32135
repeat_region	/note="A1uY repeat: matches 300. .1 of consensus" 32200. .32301 /note="A1uO repeat: matches 186. .287 of consensus incomplete repeat" 32365. .32493
repeat_region	/note="M1R repeat: matches 206. .67 of consensus" 32883. .33399 /note="M1R repeat: matches 77. .196 of consensus" 33408. .33667 /note="A1uY repeat: matches 1. .291 of consensus" 33956. .34043
repeat_region	/note="M1R repeat: matches 80. .167 of consensus" 34725. .34904 /note="A1uO repeat: matches 299. .127 of consensus incomplete repeat"

Query Match	Best Local Similarity	Score	DB	Length
repeat_L_region	34907. .35207	99.0%;	6105.4;	79376;
repeat_L_region	/note="AluI repeat: matches 300. .1 of consensus"	99.8%;	Pred. No. 0;	
repeat_L_region	35212. .35344	Matches 6165;	Conservative	0; Mismatches 1; Indels 9; Gaps 5
repeat_L_region	/note="AluIb repeat: matches 133. .1 of consensus incomplete repeat"			
repeat_L_region	36545. .36842			
repeat_L_region	/note="AluI repeat: matches 299. .1 of consensus"			
repeat_L_region	38190. .38379			
repeat_L_region	/note="MER3 repeat: matches 209. .13 of consensus"			
repeat_L_region	38382. .38682			
repeat_L_region	/note="AluX repeat: matches 1. .302 of consensus"			
repeat_L_region	38836. .38968			
repeat_L_region	/note="WIR2 repeat: matches 145. .2 of consensus"			
repeat_L_region	38983. .39279			
repeat_L_region	/note="AluIb repeat: matches 3. .296 of consensus"			
repeat_L_region	39418. .39773			
repeat_L_region	/note="THEIA repeat: matches 354. .2 of consensus"			
repeat_L_region	39775. .40120			
repeat_L_region	/note="THE1B-INTERNAL repeat: matches 1580. .1234 of consensus"			
repeat_L_region	40757. .41023			
repeat_L_region	/note="AluI repeat: matches 37. .301 of consensus incomplete repeat"			
repeat_L_region	41307. .41589			
repeat_L_region	/note="AluS repeat: matches 21. .303 of consensus"			
Query Match	99.0%;	Score 6105.4;	DB 92;	Length 79376;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 6165;	Conservative	0;	Mismatches 1;	Indels 9; Gaps 5
1	atccttgcagcttcaacctcagagcgtatatagaataaagataaaccatggaag	60		
68406	ATCTTGTTCATTTCACCTTACCTCAGGGCTATATGAAATGAATGATGATACCAATGTGAAG	68347		
61	tcctataaactatagctccatcctcgtatgctgctgcttgcagagatataaagata	120		
68346	TCCTATAAACTGTATAGCCTTCATTCGGATGATATGCTTTCGGAGATGATAAAGATGA	68287		
121	ggaagagagagatataccaagcttagccaagctgctgcagagctgctgctctatagta	180		
68286	GGAAGAGAGAGATATCCACGTTACCCAGTGTCCAGGCTGTGTCTCTTATTTTACTGA	68227		
181	cgagctgtcctcctgcagagaagctatctcttcaggaataacatcacatcaatagtaac	240		
68226	CAGATGTTCTCCTCGACAGACGATTTTCAGGAACAATCATCATCAATATGTAAATC	68167		
241	catcaaacagagagcttaagaacaagaaatgagatgagcacttgcacagaataaagctccag	300		
68166	CATCAAAACGGAGCTTAAGAAACGAGATAGAGTGGGCACTTGGCCCAAGAAAAATCCAG	68107		
301	ggagagaataatagatgaaaaataaaccttcccttctgtttttaatctcaggaataaag	360		
68106	GAGAGCAATATGATGAAAAATTAACCTTTTCCCTTTGTTTTTAATTTTCAGGAAAAATG	68047		
361	atgagagaccataatcaatgaataaagaacaagctcagaataaagaatgttccaaaatcg	420		
68046	ATGAGAGACCAAAATCAATGATTAAGAAACACGCTCAGAAAAAAGATGTTTCCAAATGCG	67987		
421	taataagatattgttctccttgggaagagacccatcagtgagcttgaatggaataatgga	480		
67986	TAAATTAAGATATTTGCTTCTTGGGAAAGACCTTCATGTGAGCTGTATGGAATAATGGGA	67927		
481	aaagcgcataaagcagatctgacacagatcccaagagtgatattatatttaaaacagat	540		
67926	AAAGCGCAAAAGCATATCTGATCAATCCCAAGAGTGATTAATTTTAAAAACAGAT	67867		
541	ggcatcacctcgggagagcaagctcaggaagtgcatgcttagcaaaagacataaacaatac	600		
67866	GGCATCACTCTGGGAGGACAGTTCCAGAAAGTCACTTAGCAAAAGACATATACATTAAC	67807		
601	agcaaaatcaaaaatctccgcaaatgcagaggaataatgaggactggaagcttcaaac	660		
67806	AGCAAAATCAAAATTCGCAAAATGACGAGGAAATGGGAGACTGGGAAAGCTTTCATTAAC	67747		

QY 661 agtgaatcaggcagcttgagcaatgcttcgcaacacccctcccgctctatacaccaggaaacacaaa 720
|||||
Db 67746 agtgaattagcagatgtagacatggttcgcaacacctcccgctctataccaggaaacacaaaa 67687
QY 721 attgacctgggctaaagccttgagcttccaaggaaatgatgaanaacttgagagcaaaacaaa 780
|||||
Db 67686 attgacacggcgcttaagccttgagcttccaaggaaatgatgaanaacttgagagcaaaacaaa 67627
QY 781 gacacagctaaagaagcaacagaaacatctgtgagccttcaagcagcagctgccccctcagca 840
|||||
Db 67626 gacattggttaaaaggcaacacgaacattgtgagccttcaaaagcagcagctgccccctcagca 67567
QY 841 gggagcccttgaggcacttgccctttagaaggccagcttctctaaaggaaatcttaagaanaatc 900
|||||
Db 67566 gggagcccttgaggcaattggccttttagaaggccagcttctttaaaggaaatcttaagaanaatc 67507
QY 901 ttgaagaatcaatgaatttcaacaaatcttaagtaaaacaataatgcgatgacataatcag 960
|||||
Db 67506 ttgcaaaagatcatgaatttttaaccatttttaagtaaaacaataatgcgatgacataatcag 67447
QY 961 tttagagacatggctcccaatttataaagtcaggaatacagaagataaagctgtccagctcc 1020
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Db 67446 tttagagacatggctcccaatttttaaaagtcaggaatacagaagataaagctgtccagctcc 67387
QY 1021 ggaataaggctcagaataatcaatagaataatcaatgcttcacacacacacacacacacacac 1080
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Db 67386 ggaataaggctcagaataatcaatagaataatcaatgcttcacacacacacacacacacacac 67327
QY 1081 tgcataatgcccctcaacacagagcccgatgtgtctgacctcaacacacacacacacacacac 1140
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Db 67326 tgcataatgcccctcaacacagagcccgatgtgtctgacctcaacacacacacacacacacac 67267
QY 1141 gtgacctcaacacacatgcttaagaagctgcatcagtagtgcacatacacaatgcccacactccc 1200
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Db 67266 gtgacctcaacacacatgcttaagaagctgcatcagtagtgcacatacacaatgcccacactccc 67207
QY 1201 tgtgacagcccatcccgcttcacacaggaagcttccccacactcagacacttctgacacacagat 1260
|||||
Db 67206 tgtgacagcccatcccgcttcacacaggaagcttccccacactcagacacttctgacacacagat 67147
QY 1261 taacagccagaagaagctcgctgagaggttgagaggtctgtctgtcttaacacacacacacacac 1320
|||||
Db 67146 taacagccagaagaagctcgctgagaggttgagaggtctgtctgtcttaacacacacacacacac 67087
QY 1321 accgtgac 1380
|||||
Db 67086 accgtgac 67027
QY 1381 cgcgttagctgggac 1440
|||||
Db 67026 cgcgttagctgggac 66967
QY 1441 gcttcaac 1500
|||||
Db 66966 gcttcaac 66907
QY 1501 agcctctcaagaagctgggac 1560
|||||
Db 66906 agcctctcaagaagctgggac 66847
QY 1561 ttaaaaggaataaacttgaatgtcttcaaaacacacacacacacacacacacacacacacacacac 1620
|||||
Db 66846 ttaaaaggaataaacttgaatgtcttcaaaacacacacacacacacacacacacacacacacacac 66787
QY 1621 taacttcaagggaatctctgggaatggggaatggggaatggggaatggggaatggggaatgggga 1680
|||||
Db 66786 taattttcaggggaattcttgagatggggaatggggaatggggaatggggaatggggaatgggga 66727
QY 1681 caactgtgcccaac 1740
|||||
Db 66726 caactgtgcccaac 66667

QY 1741 caccatgcttcttgctgaagcctccacacatcgcttactgaataaagagatatacataaactag 1800
|||||
Db 66666 caccatgcttcttgctgaagcctccacacacatcgcttactgaataaagagatatacataaactag 66607
QY 1801 ttcacattgggggac 1860
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Db 66546 tgaagcccccggagaggttccctctcagcagcagctggggaagagccctcgcgaagcccccgggctcc 66487
QY 1921 tgggtgtctcgaagac 1980
|||||
Db 66486 tgggtgtctcgaagac 66427
QY 1981 gacctgtgcttctcacttctctgtgtgactcgcttcaatccacaggaatcaatggaacatc 2040
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Db 66426 gacctgtgcttctcacttctctgtgtgactcgcttcaatccacaggaatcaatggaacatc 66367
QY 2041 taattgagtaactatactctgcagac 2100
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 5300)		
	Nguyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and		
	Polansky,J.R.		
	Gene structure and properties of TIGR, an olfactomedin-related		
	glycoprotein cloned from glucocorticoid-induced trabecular meshwork		
	cells		
JOURNAL	J Biol. Chem. 273 (11), 6341-6350		(1998)
MEDLINE	98165818		
REFERENCE	2 (bases 1 to 5300)		
AUTHORS	Nguyen,T.D., Chen,P., Chen,H. and Polansky,J.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-JUN-1997) Ophthalmology, University of California San		
	Francisco, 10 Kirkham Street, San Francisco, CA 94143-0730, USA		
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response protein"
BASE COUNT 1483 a 1152 c 1236 g 1429 t
ORIGIN

Query Match 85.98; Score 5300; DB 88; Length 5300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION AF049791
VERSION AF049791.1 GI:3065670
KEYWORDS
SEGMENT 1 of 3
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2800)
AUTHORS Fingert,J.H., Ying,L., Swiderski,R.E., Nyatuen,A.M., Arbour,N.C.,
Alward,W.L.M., Sheffield,V.C. and Stone,E.M.
TITLE Characterization and comparison of the human and mouse GLC1A
glaucoma genes
JOURNAL Genome Res. (1998) In press
REFERENCE 2 (bases 1 to 2800)
AUTHORS Fingert,J.H., Ying,L., Swiderski,R.E., Nyatuen,A.M., Arbour,N.C.,
Alward,W.L.M., Sheffield,V.C. and Stone,E.M.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-1998) Ophthalmology, University of Iowa, 200
Hawkins Drive, Iowa City, IA 52242, USA
FEATURES
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ACCESSION	AB006686		complete sequence.
VERSION	AB006686.1	GI:2828342	
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ORGANISM	Homo sapiens		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (sites)		
	Escaribano, J., Ortego, J. and Coca-Prados, M.		
	Isolation and characterization of cell-specific cDNA clones from a		
	subtractive library of the ocular ciliary body of a single normal		
	human donor: transcription and synthesis of plasma proteins		
	J. Biochem. 118 (5), 921-931 (1995)		
JOURNAL	2 (sites)		
MEDLINE	96318503		
REFERENCE	2 (sites)		
AUTHORS	Stone, E.M., Fingert, J.H., Alward, W.L., Nguyen, T.D., Polansky, J.R.,		
	Sunden, S.L., Nishimura, D., Clark, A.F., Nystuen, A., Nichols, B.E.,		
	Ritch, R., Kalenka, J.W., Craven, E.R. and Sheffield, V.C.		
	Identification of a gene that causes primary open angle glaucoma		
	science 275 (5300), 668-670 (1997)		
JOURNAL	3 (sites)		
MEDLINE	97158493		
REFERENCE	3 (sites)		
AUTHORS	Kubota, R., Noda, S., Wang, Y., Minoshima, S., Asakawa, S., Kudoh, J.,		
	Mashima, Y., Oguchi, Y. and Shimizu, N.		
	A novel myosin-like protein (myocillin) expressed in the connecting		
	cilium of the photoreceptor: molecular cloning, tissue expression,		
	and chromosomal mapping		
	Genomics 41 (3), 360-369 (1997)		
JOURNAL	4 (sites)		
MEDLINE	97312692		
REFERENCE	4 (sites)		
AUTHORS	Kubota, R., Kudoh, J., Mashima, Y., Asakawa, S., Minoshima, S.,		
	Hejtmancik, J.F., Oguchi, Y. and Shimizu, N.		
	Genomic organization of the human myocillin gene (MYOC) responsible		
	for primary open angle glaucoma (GLCIA)		
	Biochem. Biophys. Res. Commun. 242 (2), 396-400 (1998)		
JOURNAL	5 (bases 1 to 1228)		
MEDLINE	9811364		
REFERENCE	5 (bases 1 to 1228)		
AUTHORS	Shimizu, N. and Kudoh, J.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-AUG-1997) to the DDBJ/EMBL/GenBank databases.		
	Nobuyoshi Shimizu, Kelo University School of Medicine, Department		
	of Molecular Biology, 35 Shinonomachi, Shinjuku-ku, Tokyo 160-8582		
	Japan (E-mail: shimizu@mb.med.keio.ac.jp,		
	Tel: 81-3-3351-2370 (ex. 2720), Fax: 81-3-3351-2370)		
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ACCESSION	297171						
VERSION	297171.1	GI:2425156					
KEYWORDS	GLCIA.						
SOURCE	human.						
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REFERENCE	Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.						
AUTHORS	1 (bases 1 to 1086) Stone,E.M., Fingeret,J.H., Alward,W.L., Nguyen,T.D., Polansky,J.R., Sundén,S.L., Nishimura,D., Clark,A.F., Nystuen,A., Nichols,B.E., Ritch,R., Kelenak,J.W., Craven,E.R. and Sheffield,V.C.						
TITLE	Identification of a gene that causes primary open angle glaucoma						
JOURNAL	Science 275 (1997), 668-670 (1997)						
MEDLINE	97158493						
REFERENCE	2 (bases 1 to 1086) Adam,M.F., Belmouden,A., Blinist,P., Bresin,A.P., Vaitot,F., Becheuolle,A., Descotte,J.C., Coplin,B., Gomez,L., Chaventre,A., Bach,J.F. and Garchon,H.J.						
AUTHORS	Recurrent mutations in a single exon encoding the evolutionarily conserved olfactomedin-homology domain of TIGR in familial open-angle glaucoma						
TITLE	Hum. Mol. Genet. 6 (12), 2091-2097 (1997)						
JOURNAL	97472461						
MEDLINE	3 (bases 1 to 1086)						
REFERENCE	Garchon,H.J.						
AUTHORS	Direct Submission						
TITLE	Submitted (20-JUN-1997) Garchon H.-J., Hopital Necker, INSERM U25						
JOURNAL	161 rue de Sevres 75743 Paris cedex 15 FRANCE						
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shlitzu,N.
TITLE Direct Submission
JOURNAL Submitted (02-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Nobuyoshi Shlitzu, Keio University School of Medicine, Department
of Molecular Biology, 35 Shinanomachi, Shinjuku-Ku, Tokyo 160,
Japan (E-mail:shlitzu@med.keio.ac.jp, Tel:03-3351-2370,
Fax:03-3351-2370)
2 (sites)
REFERENCE
AUTHORS Kubota,R., Noda,S., Wang,Y., Minoshima,S., Asakawa,S., Kudoh,J.,
Mashima,Y., Oguchi,Y. and Shlitzu,N.
TITLE A novel myosin-like protein (myocilin) expressed in the connecting
cillum of the photoreceptor: molecular cloning, tissue expression,
and chromosomal mapping
JOURNAL Genomics 41 (3), 360-369 (1997)
MEDLINE 97312692
COMMENT On Nov 20, 1997 this sequence version replaced gi:2104213.
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RESULT 8
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LOCUS Sequence 1 from Patent WO916898.
DEFINITION AX004457
ACCESSION AX004457.1 GI:9927916
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1871)
AUTHORS Anclil,J.L. and Cote,G.
TITLE Molecular diagnosis of glaucomas associated with chromosomes 1,
and method of treatment thereof
JOURNAL Patent: WO 9916898-A 1 08-APR-1999;
ANCTIL JEAN LOUIS (CA); CORE GILLES (CA)
FEATURES
source location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 499 a 483 c 507 g 382 t
ORIGIN

Query Match 10.4%: Score 640.4; DB 9; Length 1871;
Best Local Similarity 99.8%: Pred. No. 4,5e-134;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5301 agagcttccagagagagctccacagctctcgaatgaggtctctgtgcaagctgc 5360
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Qy 5541 tcaatcattcaactttagagagagacagcagcaaccagctttagacctgagagcc 5600
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Db 601 CGAGACACTGCTCGGCTGTGCCACCGAGCTCCAGAGAGTT 642

RESULT 9
AX004474 1871 bp DNA PAT 24-AUG-2000
LOCUS Sequence 18 from Patent WO916898.
DEFINITION AX004474
ACCESSION AX004474
VERSION AX004474.1 GI:9927933
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1871)
AUTHORS Anclil,J.L. and Cote,G.
TITLE Molecular diagnosis of glaucomas associated with chromosomes 1,
and method of treatment thereof
JOURNAL Patent: WO 9916898-A 18 08-APR-1999;
ANCTIL JEAN LOUIS (CA); CORE GILLES (CA)
FEATURES
source location/Qualifiers
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CDS

BASE COUNT 499 a 483 c 507 g 382 t
ORIGIN

Query Match 10.4%: Score 640.4; DB 9; Length 1871;
Best Local Similarity 99.8%: Pred. No. 4,5e-134;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5301 agagcttccagagagagctccacagctctcgaatgaggtctctgtgcaagctgc 5360
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Db 61 TCACAGCTTTGGGCTGAGATGCCAGCTGTCCAGCTCTCTGCTGCGCTGGTGTGG 120
Qy 5421 gatgtggggcagagcagctcagctcagaagagccaaagacagagtgccgagtc 5480
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Qy 5481 tatacctcagtgctgagctcccaatgaaatccagctgcccagagagagccagctg 5540
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RESULT 10
AR030962 AR030962 1999 bp DNA PAT 29-SEP-1999
LOCUS AR030962
DEFINITION Sequence 2 from patent US 5861497.
ACCESSION AR030962
VERSION AR030962.1 GI:5944176
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1999)
AUTHORS Nguyen,T.D., Polansky,J.R. and Huang,W.
TITLE trabecular meshwork induced glucocorticoid response (TIGR) nucleic
JOURNAL Patent: US 5861497-A 2 19-JAN-1999;
FEATURES
source 1. .1999
location/Qualifiers
BASE COUNT 537 a 508 c 534 g 420 t
ORIGIN

Query Match 10.4%; Score 640.4; DB 9; Length 1999;
Best Local Similarity 99.8%; Pred. No. 4.5e-134;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5301 agagcttcagaagaaagcctcaacaaagcctctgcaatgaggtctctctgtgcagctg 5360
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Qy 5421 gatgtggggcagaagacagctcaagctcaagaaagcgaatgaagcttgagcgaatgcag 5480
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Qy 5481 tataccttcagctgtgagcagatcccaatgaaatcagctgtgcccagaagcagaagcag 5540
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RESULT 11
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LOCUS AR066022
DEFINITION Sequence 2 from patent US 5849879.
ACCESSION AR066022
VERSION AR066022.1 GI:5996238
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1999)
AUTHORS Nguyen,T.D., Polansky,J.R. and Huang,W.
TITLE Methods for the diagnosis of glaucoma
JOURNAL Patent: US 5849879-A 2 15-DEC-1998;
FEATURES
source 1. .1999
location/Qualifiers
BASE COUNT 537 a 508 c 534 g 420 t
ORIGIN

Query Match 10.4%; Score 640.4; DB 9; Length 1999;
Best Local Similarity 99.8%; Pred. No. 4.5e-134;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION	Human trabecular meshwork inducible glucocorticoid response protein (TRIGR) mRNA, complete cds.								
VERSION	085257								
KEYWORDS	085257.1 GI:2978428								
SOURCE ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
REFERENCE AUTHORS	Ngyuen,T.D. and Polansky,J.R. 1 (bases 1 to 2000)								
TITLE JOURNAL REFERENCE	Glucocortiocid effects on HRM cells: Molecular Biology Approaches Glaucoma update 4, 331-343 (1991) 2 (bases 1 to 2000) Stone,E.M., Fingerl,J.H., Alward,W.L.M., Ngyuen,T.D., Polansky,J.R., Sundem,S.L.F., Nishimura,D., Clark,A.F., Nyetuen,A., Nichols,B.E., Mackey,D.A., Ritch,R., Kalenak,J.W., Craven,E.R. and Sheffield,V.C. Identification of a gene that causes primary open angle glaucoma Science 275 (5300), 668-670 (1997) 97158493								
TITLE MEDLINE REFERENCE	3 (bases 1 to 2000) Ngyuen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and Polansky,J.R. Gene structure and properties of TRGR, an olfactomedin-related glycoprotein cloned from glucocorticold-induced trabecular meshwork cells J Biol Chem. 273 (11), 6341-6350 (1998) 98165818								
JOURNAL TITLE REFERENCE	4 (bases 1 to 2000) Ngyuen,T.D. and Polansky,J.R. Direct Submission Submitted (13-JAN-1997) Ophthalmology, University of California San Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA 5 (bases 1 to 2000) Nguyen,T.D. Direct Submision Submitted (02-APR-1997) Ophthalmology, Universly of Califofrnia San Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA Sequence update by submitter 6 (bases 1 to 2000) Nguyen,T.D. Direct Submission Submitted (19-MAR-1998) Opthalmology, University of Califfornla San Francisco, 10 Kirkham Street, San Francisco, CA 94143, USA Sequence update by submiter On Mar 19, 1998 this sequence version replaced gi:1945067.								
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BASE COUNT 538 a 508 c 534 g 420 t
ORIGIN

Query Match 10.4%; Score 640.4; DB 97; Length 2000;
Best Local Similarity 99.8%; Pred. No. 4.5e-134;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 14
AB4847 2002 bp DNA PAT 21-JAN-2000
LOCUS Sequence 2 from Patent WO9844108.
DEFINITION AB4847
ACCESSION AB4847
VERSION AB4847.1 GI:6733711
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2002)
AUTHORS Huang, W. and Nguyen, T. D.
TITLE DIAGNOSIS AND PROGNOSIS OF GLAUCOMA
JOURNAL Patent: WO 9844108-A 2 08-OCT-1998;
HUANG WEIDONG (US); NGUYEN THAI D (US)
FEATURES
source 1..2002
location/qualifiers
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/db_xref="taxon:32644"
BASE COUNT 538 a 508 c 535 g 421 t
ORIGIN

Query Match 10.4%; Score 640.4; DB 9; Length 2002;
Best Local Similarity 99.8%; Pred. No. 4.5e-134;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Job time: 14966 sec

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RESULT 15
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DEFINITION Sequence 2 from Patent WO9844107.
ACCESSION A84850
VERSION A84850.1 GI:5733713
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2000)
AUTHORS Huang, W. and Nguyen, T. D.
TITLE DIAGNOSIS AND PROGNOSIS OF GLAUCOMA
JOURNAL Patent: WO 9844107-A 2 08-OCT-1998;
UNIVERSITY OF CALIFORNIA (US); HUANG WEIDONG (US)
FEATURES
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/organism="unidentified"
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BASE COUNT 538 a 506 c 534 g 422 t
ORIGIN

Query Match 10.3%; Score 635.6; DB 9; Length 2000;
Best Local Similarity 99.4%; Pred. No. 5.4e-133;
Matches 638; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5301 agagcttcacagagagagcctcaccaagcctctgcattgaggttctctgtcagcttgc 5360
DB 1 ACAGCTTTCAGAGAGAGAGCCTCACCAAGCCTCTGCATGAGGTCTTGTGTGACGCTGC 60
OY 5361 tgcagcttgggacctgaga tgcagcttgcagcttgcagcttgccttgcctgctgtgtg 5420
DB 61 TGCAGCTTGGGCGCTGAGATGCCAGCTGTCAAGCTGTCTGTGCGCTGCGCTGTGTGG 120
OY 5421 gattgtggggccagagacagctcagctcagaagggccaatgacccaagtgccgatgccag 5480
DB 121 GATGTGGGGGCCAGGACAGCTCAGCTCAGCAAGGCGCAATGACCAAGTGGCGGATGCCAG 180
OY 5481 tatccttcagcttgcagcttgcacaaatgaatcagcttgcagagcagagccagagccatg 5540
DB 181 TATACCTTACGTGTGGCCAGTCCCAATGAATCCAGCTGCCACAGAGAGCCAGGCCATG 240
OY 5541 tcaatcatalaacttacagagagacagcagcaccacagcttagaccttgaggccacc 5600
DB 241 TCAGTCATTCATTAAGTACAGAGAGACAGCACCCACCAACGCTTAGACCTGGAGGCCACC 300
OY 5601 aaagctgacatcagctcccttgaggagccctccacaaatgaaccttggaccagctgcc 5660
DB 301 AAGCTCGACTGAGCTCCCTGGAGAGCCTCTTCACCAATTGACCTTGAGACCAGGCTGCC 360
OY 5661 aggccccagagagagagagagggctgcagagagagcctgagccctgagggagagcgg 5720
DB 361 AGGCCCAAGAGACCCAGAGAGGCGCTGCAGAGGAGAGCTGGCACCCTTGAGCGGGAGCGG 420
OY 5721 gaccagctggaaacccaacacagagagttgagagcttgcctacagcaacctcctccgagac 5780
DB 421 GACCAAGCTGGAACCAACCAACAGAGAGTTGGAGACTGCCTACAGCAACCTCCTCCGAGAC 480
OY 5781 aagtcagttcttggagagagagagagagcactaagcagaagaatgagaatctggccag 5840
DB 481 AAGTCAGTTCTTGAGAGAGAGAGAGAGAGGACACTTAAGGCAAGAAATGAGAAATCTGGCCAGG 540
OY 5841 aggttggaaagcagcagcagagaggttagcaagctgagaaaggccagtgctccagacc 5900
DB 541 AGGTTGGAAGACAGACAGCAGAGAGGTACCAAGGCTGAGAGAGGGGCCAGGTCCAGTACC 600
OY 5901 cgagacactgctcgggctgtgcacacaggtccacagagagtt 5942
DB 601 CGAGACACTGCTCGGGCTGTGCCACACAGGCTCCAGAGAGTT 642
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